Amendments to Claims

Claim 1. (Withdrawn) A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a gene selected from the group consisting of: a *nrtA* gene and a *glnB* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) in the presence of nitrate wherein the chimeric gene is expressed.

Claim 2. (Withdrawn) A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a *glyoxII* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) at a pH of about 5.5 wherein the chimeric gene is expressed.

Claim 3. (Withdrawn) A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a *htpG* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) at a temperature suitable for induction of the promoter region wherein the chimeric gene is expressed.

Claim 4. (Withdrawn) A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a gene selected from the group consisting of: a *moxF* gene and a *hps* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria; wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) in the presence of a C1 carbon source selected from the group consisting of methane and methanol wherein the chimeric gene of step (a) is expressed.

Claim 5. (Withdrawn) A method according to any of Claims 1-4 wherein the C1 metabolizing bacterial host cell is selected from the group consisting of methanotrophs and methylotrophs.

Claim 6. (Withdrawn) A method according to Claim 5 wherein the C1 metabolizing bacterial host cell is a methylotroph selected from the group consisting of *Methylomonas, Methylobacter, Mehtylococcus, Methylosinus, Methylocyctis, Methylomicrobium, Methanomonas, Methylophilus, Methylobacillus, Methylobacterium, Hyphomicrobium, Xanthobacter, Bacillus, Paracoccus, Nocardia, Arthrobacter, Rhodopseudomonas,* and *Pseudomonas.*

Claim 7. (Withdrawn) A method according to Claim 1 wherein the promoter region has the nucleic acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:6.

Claim 8. (Withdrawn) A method according to Claim 2 wherein the promoter region has the nucleic acid sequence as set forth in SEQ ID NO:9.

Claim 9. (Withdrawn) A method according to Claim 3 wherein the promoter region has the nucleic acid sequence as set forth in SEQ ID NO:12.

Claim 10. (Withdrawn) A method according to Claim 3 wherein the temperature suitable for induction of the promoter region is selected from the group consisting of:

a) 41-42°C wherein the C1 metabolizing bacteria is mesophilic; and

b) 47-50°C wherein the C1 metabolizing bacteria, is thermophilic

Claim 11. (Withdrawn) A method according to Claim 4 wherein the nucleic acid fragment comprising the promoter region has the nucleic acid sequence selected from the group consisting of SEQ ID NO:15, and 18.

Claim 12. (Withdrawn) A method according to Claim 1 wherein the concentration of nitrate is from about 5mM to about 15mM.

Claim 13. (Withdrawn) The method according to any one of Claims 1 – 4 wherein the coding region of interest is selected from the group consisting of genes encoding: transaldolase, fructose bisphosphate aldolase, keto deoxy phosphogluconate aldolase, phosphoglucomutase, glucose-6-phosphate isomerase, phosphofructokinase, 6-phosphogluconate dehydratase, 6-phosphogluconate-6-phosphate-1 dehydrogenase, *dxs, dxr, ispA, ispD, ispE, ispF, crtE, crtX, crtY, crtI, crtB, crtZ, crtD, crtO, crtW,* genes encoding

limonene synthase, *ugp, gumD, wza, espB, espM, waaE, espV, gumH,* genes encoding glycosyltransferase genes, *aroG, aroB, aroQ, aroE, aroK,* 5-enolpyruvylshikimate-3-phosphate synthase, *aroC, trpE, trpD, trpC , trpB, pheA, tyrAc, pds, phaC, phaE, efe, pdc, adh,* pinene synthase, bornyl synthase, phellandrene synthase, cineole synthase, sabinene synthase, and taxadiene synthase.

Claim 14. (Withdrawn) A method for the production of zeaxanthin comprising:

a) providing a transformed C1 metabolizing host cell comprising:
   1) suitable levels of b-Carotene; and
   2) a chimeric gene comprising the promoter region of the *hps* gene operably linked to a coding region encoding β-carotene hydroxylase; and

(b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby an zeaxanthin is produced.

Claim 15. (Currently Amended). An isolated nucleic acid molecule encoding a nitrate inducible gene selected from the group consisting of:

(a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NO:2 ~~and SEQ ID NO:5~~;

(b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

Claim 16. (Currently Amended). The isolated nucleic acid molecule of Claim 15 ~~selected from the group consisting of~~as set forth in SEQ ID NO:1 ~~and SEQ ID NO:4.~~

Claim 17. (Withdrawn) A polypeptide encoded by the isolated nucleic acid molecule of Claim 15.

Claim 18. (Withdrawn) The polypeptide of Claim 17 selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:5.

Claim 19. (Currently Amended). An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a nrtA enzyme of at least 464 amino acids that has at least ~~70~~90% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:2;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

Claim 20. (Withdrawn) An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a glnB enzyme of at least 112 amino acids that has at least 76% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:5;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

Claim 21. (Withdrawn) An isolated nucleic acid molecule encoding a pH inducible gene selected from the group consisting of:

a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:8;

b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or

an isolated nucleic acid molecule that is complementary to (a), or (b).

Claim 22. (Withdrawn) The isolated nucleic acid molecule of Claim 21 as set forth in SEQ ID NO:7.

Claim 23. (Withdrawn) A polypeptide encoded by the isolated nucleic acid molecule of Claim 21.

Claim 24. (Withdrawn) The polypeptide of Claim 23 having the amino acid seqeunce as set forth in SEQ ID NO:8.

Claim 25. (Withdrawn) An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a glyoxII enzyme of at least 231 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:8;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

Claim 26. (Withdrawn) An isolated nucleic acid molecule encoding a temperature inducible gene selected from the group consisting of:

a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:11;

b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

Claim 27. (Withdrawn) The isolated nucleic acid molecule of Claim 26 as set forth in SEQ ID NO:10.

Claim 28. (Withdrawn) A polypeptide encoded by the isolated nucleic acid molecule of Claim 26.

Claim 29. (Withdrawn) The polypeptide of Claim 28 having the amino acid sequence as set forth in SEQ ID NO:11.

Claim 30. (Withdrawn) An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a htpG enzyme of at least 644 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:11;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

Claim 31. (Withdrawn) An isolated nucleic acid molecule encoding a methane or methanol inducible gene selected from the group consisting of:

(a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NO:14, and 17;

(b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

Claim 32. (Withdrawn) The isolated nucleic acid molecule of Claim 31 selected from the group consisting of SEQ ID NO:13, and 16.

Claim 33. (Withdrawn) A polypeptide encoded by the isolated nucleic acid molecule of Claim 31.

Claim 34. (Withdrawn) The polypeptide of Claim 33 selected from the group consisting of SEQ ID NO:14, and 17.

Claim 35. (Withdrawn) An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a moxF enzyme of at least 89 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:14;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

Claim 36. (Withdrawn) An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a hps enzyme of at least 215 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:17;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

Claim 37. (Withdrawn) A promoter region responsive to the presence of nitrate having the nucleic acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:6.

Claim 38. (Withdrawn) A promoter region responsive to acidic pH having the nucleic acid sequence as set forth in SEQ ID NO:9.

Claim 39. (Withdrawn) A promoter region responsive to elevated temperatures having the nucleic acid sequence as set forth in SEQ ID NO:12.

Claim 40. (Withdrawn) A promoter region highly expressed in the presence of methane or methanol having the nucleic acid sequence selected from the group consisting of SEQ ID NO:15, and SEQ ID NO:18.